## AMENDMENTS TO THE CLAIMS

1.-37. (Canceled)

38. (Previously presented) The method of claim 111 wherein said nucleic acid target is RNA.

39. (Previously presented) The method of claim 111 wherein said nucleic acid target comprises RNA and one or more deoxynucleotides at preselected locations.

40.-94. (Canceled)

95. (Previously presented) The method of claim 111, wherein each member of said mixture of compounds is an oligonucleotide.

96. (Canceled)

97. (Previously presented) The method of claim 111, wherein each member of said mixture of compounds is a small molecule.

98. (Previously presented) The method of claim 38, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (Previously presented) The method of claim 112, wherein each member of said mixture of compounds is an oligonucleotide.

100. (Canceled)

101. (Previously presented) The method of claim 112, wherein said nucleic acid target is RNA.

102. (Canceled)

103. (Previously presented) The method of claim 101, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104. (Previously presented) The method of claim 112, wherein each member of said mixture of compounds is a small molecule.

105.-108. (Canceled)

109. (Previously presented) The method of claim 38, wherein said RNA comprises a molecular interaction site.

110. (Previously presented) The method of claim 101, wherein said RNA comprises a molecular interaction site.

111. (Currently Amended) A method comprising

(a) selecting a nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair;

(b) forming a complex comprising a standard binding compound and said nucleic acid target, wherein the complex has a known ion abundance and mass to charge ratio;

(c) combining ~~with~~ said complex **with** a mixture of **known** compounds under competitive binding conditions;

(d) subjecting said combination of step (c) to mass spectrometry;

(e) collecting mass spectral data for said combination, wherein said mass spectral data provides an ion abundance and mass to charge ratio for a plurality of ions;

(f) comparing at least one mass to charge ratio obtained in step (e) to the known mass to charge ratio of the complex to determine whether binding of one or more members of said mixture of **known** compounds to the nucleic acid target has occurred; and

(g) calculating the mass of said one or more members to determine the identity of said one or more members **of said mixture of known compounds**.

112. (Currently Amended) A method comprising

(a) forming a complex of a nucleic acid target and a standard binding compound, wherein the nucleic acid target comprises at least one loop, bulge, kink, stem structure, or mismatched base pair;

(b) subjecting said complex to mass spectrometry;

(c) collecting mass spectral data for said complex, wherein the mass spectral data provides an ion abundance and a mass to charge ratio for an ion of the complex;

(d) combining said complex with a mixture of **known** compounds under competitive binding conditions;

(e) subjecting said combination of step (c) to mass spectrometry;

(f) collecting mass spectral data for said combination, wherein said mass spectral data provides an ion abundance and mass to charge ratio for one or more of a plurality of ions;

(g) comparing the mass to charge ratio collected in steps (c) and (f), to determine whether binding of one or more members of the mixture of **known** compounds to the nucleic acid target has occurred; and

(h) calculating the mass of said one or more members to determine the identity of said one or more members **of said mixture of known compounds.**

113. (Previously Presented) The method of claim 111, further comprising comparing the ion abundance of said one or more members to the known ion abundance of the complex to determine a relative dissociation constant for said member, thereby determining binding affinity of said member for said nucleic acid target.

114. (Previously Presented) The method of claim 112, further comprising comparing the ion abundance of said one or more members to the known ion abundance of the complex to determine a relative dissociation constant for said member, thereby determining binding affinity of said member for said nucleic acid target.